

Aspergillus fumigatus NMT

1 ATGGCGGAGTCGCTATTGGAAAACAAACCCCGCTCTCAGGAACGAGACGGCGGCATGGACAAAAGACAAAGCGGCGGAGGCAATGCGCAAAATGACATTG 100
M A E S L L E N P A L R N E T A G M D K D K A E A M R K M N I A

101 CCGAATTGCTGACAGGCTTGTCAGTTCCGGGAAGAACCAGAAGGATATGGCTTCGTACAAGTTTGGCAACGCGAGCCTGTGCCCGGATTGCGATGAGAC 200
E L L T G L S V S G K N Q K D M A S Y K F W Q T Q P V P R F D E T

201 GAGTACCGATACCTGGGGCCCTATCAAGATCATTGATCCTGAAAGGTCTCAAGGAACCGGATGCGCTGTTCAAGGATTGGAATGGGCGACATCGAC 300
S T D T G G P I K I I D P E K V S K E P D A L L E G F E W A T L D

301 CTGACAAAACGAGACTGAGCTGCAGGAGCTGTGGGATTGTTGACGTATCACTACGTAGAGGACGACAATGCCATGTTCCGGTTCAGATATTGCGAGTCGT 400
L T N E T E L Q E L W D L L T Y H Y V E D N A M F R F R Y S Q S F

401 TCCTACACTGGGCTCTTATGTCGCTGGCTGGAAAAGGAATGGCATGTCCGCTACGAACTCGCGCAACTGGTAGCGTCCCATTTGCGGTGT 500
L H W A L M S P G W K K E W H V G V R A T K S R K L V A S I C G V

501 CCGGACAGAGATCAATGTGGCAATCAAAAGCTCAAGGTGTCGAGATCAATTTCTCTGCATCCACAAGAAGCTCCGCTCGAAGCGCTTGACCCCAAGTT 600
P T E I N V R N Q K L K V V E I N F L C I H K K L R S K R L T P V

601 CTCATCAAGAATAACCCGTCGTTGTACTCAATGGCATCTACCAAGCCATCTACACTGGGGGTGTGGTGTCTCCCACTCTCTGTCAGCTCATGCCGCT 700
L I K E I T R R C Y L N G I Y Q A I Y T A G V V L P T P V S S C R Y

FIG. 1A

701	ACTACCACCGTCCTTTGGACTGGTTGAAGCTTTACGAGGTGGGTTCTCGCCTCTCCCTGCCGATCCACCAAGCGCGCAGATCACCAAGAATCACCT Y H R P L D W L K L Y E V G F S P L P A G S T K A R Q I T K N H L	800
801	GCCAGTACTACTCTACCCCGGTCTTCGCCCCCATGGAGCCCAAGACATTGACACAGTGCATGATCTTTGCAGCGATACTTGTGCGGTTTGCCTTG P S T T S T P G L R P M E P K D I D T V H D L L Q R Y L S R F A L	900
901	AACCAGGCCTTTACGCGAGAGGAAGTGGACCATTGGCTCGTGCCACCAAGCGGAGACGGTCAAAAGAGCAGTCGTCTGGGCATACGTGGTAGAGGACCCCTG N Q A F T R E E V D H W L V H K P E T V K E Q V V W A Y V V E D P E	1000
1001	AAACGCACAAGATCACCGACTCTCTTTTCCTTCTACAACCTCGAATCCACCGTCATTTCAGATCCCAAGCATGACAATGTGCGTGTCTTACCTGTACTA T H K I T D F F S F Y N L E S T V I Q N P K H D N V R A A Y L Y Y	1100
1101	CTATGCACCGAAACAGCTTTCACCAATAACATGAAGGCTCTCAAGAGCGTCTGTGATGTGATGAATGACGCTCTGATCCTGGCTAAGAAGCGGCAC Y A T E T A F T N N M K A L K E R L L M L M N D A L I L A K K A H	1200
1201	TTTGATGTGTTCAACGCACTTACGCTTCACGATAAACCTCTGTTCCTCGAACAACTCAAATTTTGAGCTGGCGATGGCAGCTTCACCTTCTACCTCTACA F D V F N A L T L H D N P L F L E Q L K F G A G D G Q L H F Y L Y N	1300
1301	ACTATCGCACCGCCCTGTCTTCCTGGAGGAGTTAACGAGAAGAACCTGCCGATGACAAAAGAATGGAGGCGTTGGCATCGTTATGCTGTAA Y R T A P V P G G V N E K N L P D E K R M G G V G I V M L *	1392

FIG. 1B

nm1 (Aspergillus fumigatus)

1	TCCGACTCTAAGGATCGCAAGGGCAAGGGCCCCCGAGGGCCAGTCTTCCGAAAAGAAAGATGGCGCGGTGAACATAACCCCTCAGATCGCGGAGTCGCTAT AGGCTGAGATTCTAGCGTTCCGGGCTCCGGTCCAGAAAGCTTTTCTACCGCGCACTTGATTGGGAGTCTACCGCTCAGCGGATA	6	M A E S L L
101	TGGAAAACAACCCCGCTCTCAGGAACGAGACGGCCGGCATGGAACAAGACAAGGGCGGAGGCAATGCGCAAAATGAACATTTGCCGAATTGCTGACAGG ACCTTTTGTGGGGGAGAGTCTTCTCTGCTGCGGCGGTACCTGTTCTGTTCGGCGCCTCGGTTACGGGTTTTACTTTGTAACGGCTTAACGACTGTCC	200	
300	CTTGTCAAGTTTCGGGAAGAACCGAAGGATATGGCTTTCGTACAAGTTTGGCAAAACGACGCCCTGTGCCCGATTTCGATGAGACGAGTACCGATACTGGG GAACAGTCAAAGGCCCTTCTTGCTCTCCATACCGAAGCATGTTCAAACCGTTTCGGTCCGACACGGGCTAAGCTACTCTGCTCATGGCTATGACCC	72	
400	GGCCCTATCAAGATCATTTGATCCTCAAAAGGTCTCAAAGGAACCGGATCGGTGCTTGAAGGATTTGAATGGCGCACACTCGACCTGACAAACGAGACTG CCGGGATAGTTCTAGTAACTAGGACTTTTCCAGAGTTTCTTGCCCTACGGCAGCAACTTCTTAAACTTACCGCTGTGAGCTGGAAGTGTGCTCTGAC	106	
500	AGCTGCAGGAGCTGTGGGATTGTTGACGTATCACTACGTAGAGGACGACAAATGCCATGTTCGGTTTCAGATATTCGCAGTTCGTTCCCTACACTGGTGGGT TCGACGTCTCGACACCCCTAAACAACCTGCATAGTGATGCATCTCCTGCTGTACGGTACAAAGGCCAAGTCTATAAGCGCTCAGCAAGGATGTGACCAACCCA	137	
600	GCACAAACCGGCGGAGGATCTGTTCTCACCGGCTTGGAGGCTGCGATTATTGAGCGCTGACAAATTTGACCGGTAGGCTCTTATGTGCGCTGGCT CGTGTTCGCGCGCTCCCTAGACAAAGAGTGGCGCAACCCCTCCACACCTAATAAACTCGCGACTGTTAAACTGCCATCCCGAGATACAGCGGACCGGA	144	A L M S P G W

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601	GGAAAAAGGAATGGCATGTGCGGTGTCGCGGCTACGAAGTCGCGCAAACTGGTAGGTCCATTTCGGGTGCCGACAGAGATCAATGTGCGCAATCAAAA CCTTTTTCCTTACCGTACAGCCACAGCGCGGATGCTTCAGCGCGTTTCACCAATCGCAGGTAAACGCCACAGGGCTGTCTCTAGTTACACGCGTTAGTTT	700
145	K K E W H V G V R A T K S R K L V A S I C G V P T E I N V R N Q K	177
701	GCTCAAGGTGTCGAGATCAATTTCTCTGCCATCCACAAGAGCTCCGCTCGAAGGCTTGACCCCACTTGCATCAAGAANAATCACCCGTGCTTGCTAC CGAGTTCACGACGCTCTAGTTAAAGGAGAGCTAGGTGTTCTTCGAGCGGAGCTTCGCGAACTGGGGTCAAGAGTAGTTTCTTTAGTGGGCGAGCAACGATG	800
178	L K V V E I N F L C I H K K L R S K R L T P V L I K E I T R R C Y	210
801	CTCAATGGCATCTACCAAGCCATCTPACATCGCGGGTGTGGTCTCCCACTCTCTGTCAGCTCATGCGGCTACTACCA.CCGTCTCTTTGGA.CTGTTGAAGC GAGTTACCGTAGATGTTTCGCTAGATGTGACGCCACACACGAGGGGTGAGGACATGTCGAGTACGGCGATGATGGTGGCAGGAAACCTGACCAACTTCG	900
211	L N G I Y Q A I Y T A G V V L P T P V S S C R Y Y H R P L D W L K L	244
901	TTTACGAGTGGGTTCTCGCTCTCCCTGCCGATCCACCAAGGCGCGCAGATCAACGAATCACCTGCCCACTACTACCTCTACCCCGGCTCTTCG AAATGCTCCAGCCGAAGCGGAGAGCGGCTAGGTGGTTCGCGCGGTCTAGTGTCTTAGTGAGCGGTCTAGTGGAGATGGGGCCAGAAAGC	1000
245	Y E V G F S P L P A G S T K A R Q I T K N H L P S T T S T P G L R	277
1001	CCCATGAGCCCAAGACATTTGACACAGTGCATGATCTTTTGCAGCGATCTTTGCGGGTTTGGTTGAACCAAGGCTTTACCGGAGAGGAAGTCGAC GGGGTACCTCGGGTTCTGTAACTGTGTACGCTACTAGAAACGTCGCTATGAACAGGCCCAACCGCAACTTGGTCCGGAATCGCTCTCTTCACCTG	1100
278	P M E P K D I D T V H D L L Q R Y L S R F A L N Q A F T R E E V D	310
1101	CATTGGCTCGTCACAAGCCGAGACCGTGAAGAGCAGGTGCTCTGGGCATACGTGGTAGAGGACCTTGAACGCACAAAGATCACCGACTCTTTTCTCT GTAACCGAGCACGTGTTCGGCTCTGCCACTTCTCGTCCAGCAGACCCGTAATGCACCACTCTCTGGGACTTTGCGGTGTCTAGTGGCTGAAGAAAAGGA	1200
311	H W L V H K P E T V K E Q V V W A Y V V E D P E T H K I T D F F S F	344
1201	TCTACAACCTCGAATCCACCGTCAATTCAGAAATCCCAAGCATGCAAAATGTCGGTGTCTTACCTGTACTACTATGCAACCGGAAACAGCTTTTCACCAATAA AGATGTTGGAGCTTAGTGGCAGTAAGTCTTAGGGTTCGTACTGTACACGACCGAATGACATGATGATACGTTGGCTTTGTGGAAGTGGTTATT	1300
345	Y N L F S T V I Q N P K H D N V R A A Y L Y Y A T E T A F T N N	377

FIG. 2B

1301	CATGAAGGCTCTCAAAGAGCGTCTGCTGATGCTGATGAATGACCGCTCTGATCTGGCTAAGAAGGTAACCTACAGGATCCACTGCCATTTCCTCCCTGGAGTT GTACTTCGGAGAGTTTCTCGCAGACGACTACGACTACTTACTCGGAGACTAGGACCGATTCTCCATTGATGTCCCTAGGTGACGGTAAGGGACCTCAA	1400
378	M K A L K E R L L M L M N D A L I L A K K A	399
1401	GACTTACGAAGCTTGACATTGTGTGTGATAGCGCACTTTGATGTTCACCGCACTTAGCCTTACGATAACCCCTCTGTTCTCGAACAACTCAAAATTGG CTGAATGCTTCGACTGTAACACAACTATCCGCGTGAACTACACAAAGTTGCGTGAATGCGAAGTGCTATTGGGAGACAAAGGAGCTTGTGAGTTTAAACC	1500
400	H F D V F N A L T L H D N P L F L E Q L K F G	422
1501	AGCTGGCGATGGGAGCTTCACTTCTACCTTACAACCTATCGCACCGCCCTGTTCTCGAGGAGTTAACGAGAAGAACCTGCCGGATGAGAAAAGAAATG TCGACCGCTACCCGTCGAAGTGAAGATGGAGATGTTGATAGCGTGGCGGGGACAAAGGACTCCTCAATGCTTCTTGGACGGCTACTCTTTTCTTAC	1600
423	A G D G Q L H F Y L Y N Y R T A P V P G G V N E K N L P D E K R M	455
1601	GGAGGGTTGGCATCGTTATGCTGTAAAAACAATCTCACCGCATGGACCAATGCCCTCTCGCCTGTTGATGATCGCATCTTATACCTATTCTCGCTGTGAC CCTCGCAACCGTAGCAATACGACATTTTGTAAAGAGTGGCGTACCTGGTACGGAGAGCGGAGCAACTACTAGCGTAGAATATGGATAAGAGCGACACTG	1700
456	G G V G I V M L *	463
1701	ATGAATTGGGTATGCGAAATACCATGAAATTTG TACTTAAACCCATAGCTTTTATGGTACTTTTAAAC	

FIG. 2C

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